```
             10          30         50
-88  GTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTTCCGGGCTCTGGAGGAGGGT -29


             70          90        110
-28  CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGGGGCCGTCGCTCCACGTCT   31
-8                                 M  A  W  L  G  A  S  L  H  V  W  11


            130         150        170
 32  GGGGTTGGCTAATGCTCGGCAGCTGCCTCTGGCCAGAGCCCAGCTGGATTCTGATGGCA  91
 12   G  W  L  M  L  G  S  C  L  L  A  R  A  Q  L  D  S  D  G  T  31


            190         210        230
 92  CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCAGAAGTACAATGTGAACTCA 151
 32   I  T  I  E  E  Q  I  V  L  V  L  K  A  K  V  Q  C  E  L  N   51


            250         270        290
152  ACATCACAGCTCAACTTCCAGGAGGGAGAAGGTAATTGTTCCCTGAATGGGATGGACTCA 211
 52   I  T  A  Q  L  Q  E  G  E  G  N  C  F  P  E  W  D  G  L  I   71


            310         330        350
212  TTTGTTGGGCCCAGAGAGGAACAGTGGGGAAAAATATCGGCTGTTCCATGCCCTCTTATATTT 271
 72   C  W  P  R  G  T  V  G  K  I  S  A  V  P  C  P  P  Y  I  Y   91


            370         390        410
272  ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAACCCCAATGGAACATGGGATT 331
 92   D  F  N  H  K  G  V  A  F  R  H  C  N  P  N  G  T  W  D  F  111

     MATCH WITH FIG. 1B
```

FIG.1A

MATCH WITH FIG. 1A

```
              430            450            470
332  TTATGCACAGCTTAAATAAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTTCTGCAGC  391
112   M  H  S  L  N  K  T  W  A  N  Y  S  D  C  L  R  F  L  Q  P  131

              490            510            530
392  CAGATATCAGCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG  451
132   D  I  S  I  G  K  Q  E  F  C  E  R  L  Y  V  M  Y  T  V  G  151

              550            570            590
452  GCTACTCCATCTCTTTGGTTCCTTGGCTGTGTGGCTATTCTCATCATTGGTTACTTCAGAC  511
152   Y  S  I  S  F  G  S  L  A  V  A  I  L  I  I  G  Y  F  R  R  171

              610            630            650
512  GATTGCATTGCACTAGGAACTATATCCACACATGCACTTATTGTGTCTTTCATGCTGAGAG  571
172   L  H  C  T  R  N  Y  I  H  M  H  L  F  V  S  F  M  L  R  A  191

              670            690            710
572  CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG  631
192   T  S  I  F  V  K  D  R  V  V  H  A  H  I  G  V  K  E  L  E  211

              730            750            770
632  AGTCCCTAATAATGCAGGATGACCACCAAAAATTCCATTGAGGCAACTTCTGTGGACAAAT  691
212   S  L  I  M  Q  D  D  P  Q  N  S  I  E  A  T  S  V  D  K  S  231

              790            810            830
```

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

692 CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTATTACTTCCTGGCTACAAATT 751
232 Q Y I G C K I A V V M F I Y F L A T N Y 251

752 ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTT 811
252 Y W I L V E G L Y L H N L I F F V A F F S 271

812 CGGACACCAAATACCTGTGGGGGCTTCATCTTGATAGGCTGGGGGTTCCAGCAGCATTTG 871
272 D T K Y L W G F I L I G W G F P A A F V 291

872 TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACTTAGTG 931
292 A A W A V A R A T L A D A R C W E L S A 311

932 CTGGAGACATCAAGTGGATTATCAAGCACCACCGATCTTAGCAGCTATTGGGCTGAATTTA 991
312 G D I K W I Y Q A P I L A A I G L N F I 331

992 TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG 1051
332 L F L N T V R V L A T K I W E T N A V G 351

1052 GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCCTGGTCCTAG 1111
352 H D T R K Q Y R K L A K S T L V L V L V 371

MATCH WITH FIG. 1D

FIG.1C

MATCH WITH FIG. 1C

```
              1210          1230          1250
1112 TCTTTGGAGTGCATTACATCGTGTTCGTGTGCCTGCCTCACTCCTTCACTGGGCTCGGGT 1171
 372  F   G   V   H   Y   I   V   F   V   C   L   P   H   S   F   T   G   L   G   W  391

              1270          1290          1310
1172 GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTCAGGGTTTCTTTGTGTCTA 1231
 392  E   I   R   M   H   C   E   L   F   F   N   S   F   Q   G   F   F   V   S   I  411

              1330          1350          1370
1232 TCATCTACTGCTACTGCAATGGAGAGGTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT 1291
 412  I   Y   C   Y   C   N   G   E   V   Q   A   E   V   K   K   M   W   S   R   W  431

              1390          1410          1430
1292 GGAATCTCTCCGTGGACTGGAAAAGGACACCGGCCATGTGGCAGCCGCAGATGCGGCTCAG 1351
 432  N   L   S   V   D   W   K   R   T   P   P   C   G   S   R   R   C   G   S   V  451

              1450          1470          1490
1352 TGCTCACCACCGTGACGCACCACAGCCAGTCACAGGTGGGCAGCAGCACACGCAT 1411
 452  L   T   T   V   T   H   S   T   S   S   Q   S   Q   V   A   A   A   H   A   W  471

              1510          1530          1550
1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC 1471
 472  C   L   S   L   A   K   L   P   R   S   P   A   D   S   L   T   A   T   S   L  491
```

MATCH WITH FIG. 1E

FIG.1D

MATCH WITH FIG. 1D

```
                1570          1590            1610
1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACTTCTCCACGA 1531
 492  Y  L  A  M  S  G  V  T  Q  S  R  T  A  S  H  T  L  S  T  R   511

                1630          1650            1670
1532 GGAGCAACAAGGAAGAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCA 1591
 512  S  N  K  E  D  S  G  R  Q  R  D  D  I  L  M  E  K  P  S  R   531

                1690          1710            1730
1592 GGCCTATGGAATCTAACCCAGACACACTGAAGGATGACAAGGAGAGAAACTGAGGATGTTCTCT 1651
 532  P  M  E  S  N  P  D  T  E  G                                541

                1750          1770            1790
1652 GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC 1711

                1810          1830            1850
1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA 1771

                1870          1890            1910
1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAAATGCAAG 1831

                1930          1950            1970
1832 TGTCAATGGAGTAGTTATTACCTTCTATTGGCATCAAGTTTCCCTCTAAATTAATGTAT 1891

                1990
1892 GGTATTTGCTCTGTGATTGTTCA 1914
```
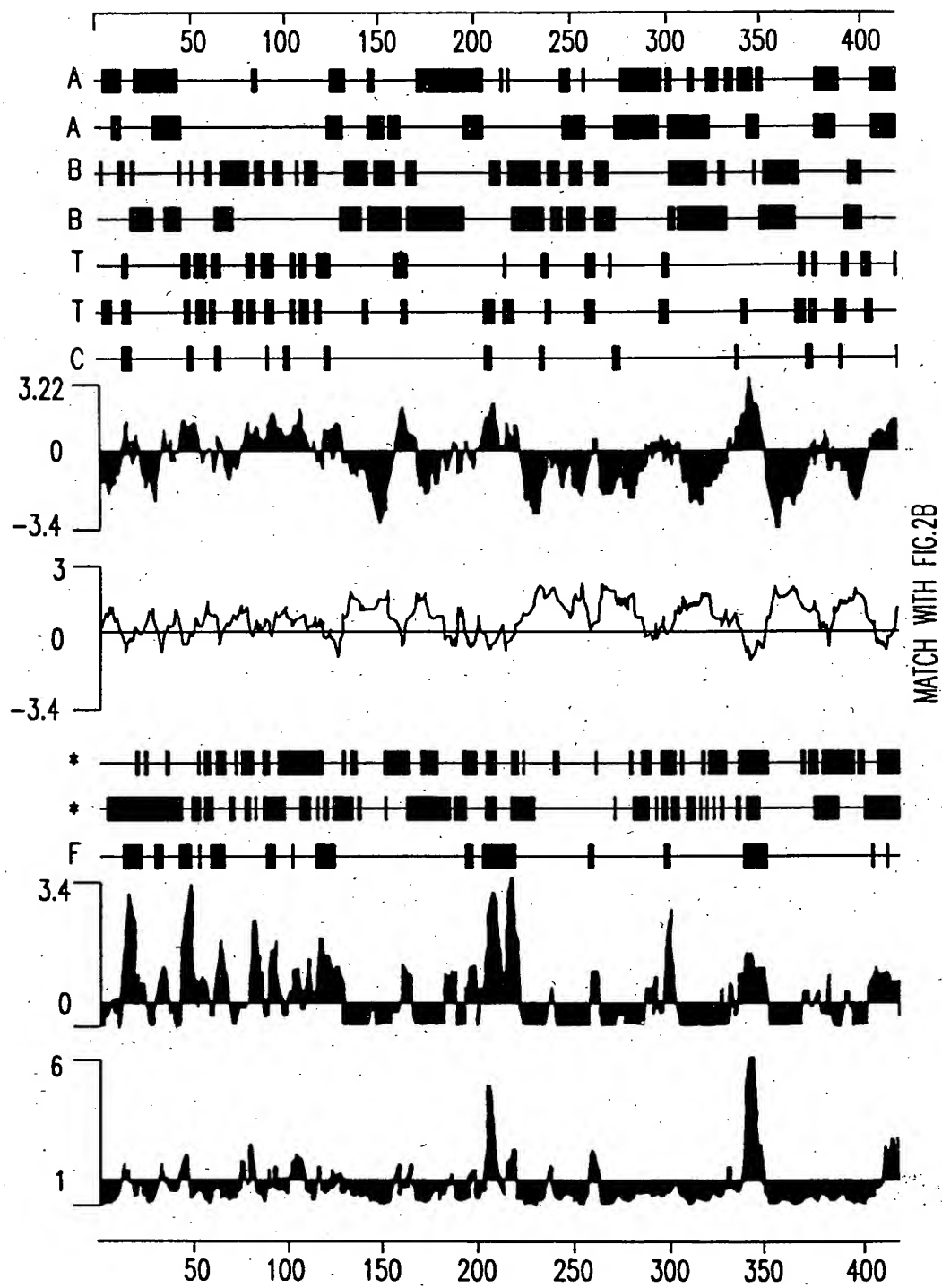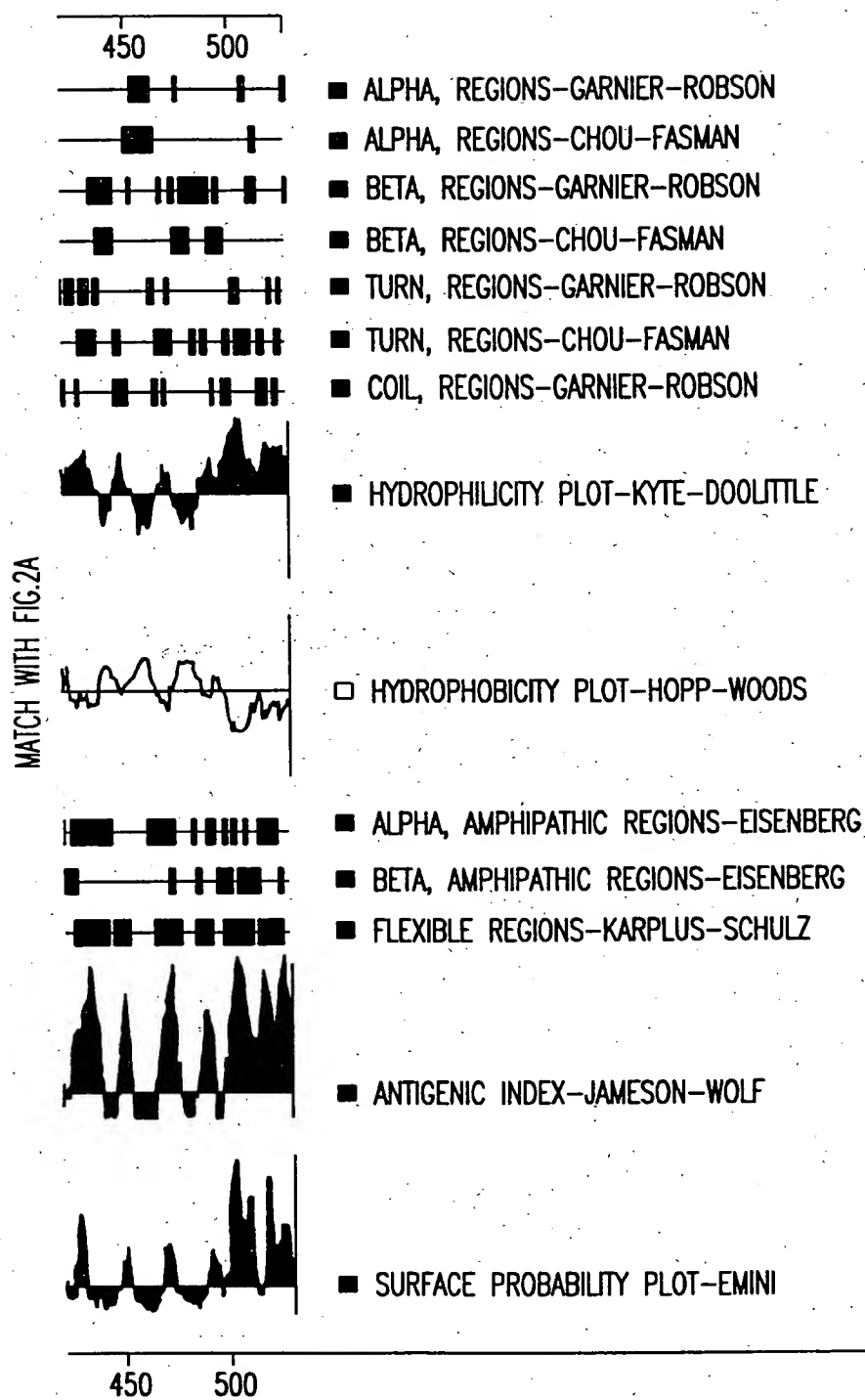
FIG.1E

MATCH WITH FIG.2B

FIG. 2A

FIG.2B

Sequences producing High-scoring Segment Pairs:

	Reading Frame	High Score	Probability P(N)	N
gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir|S|A39286 parathyroid hormone / parathyroi...	+3	597	2.9e-203	6
gp|L04308|HUMPTHR_1 parathyroid hormone receptor [Ho...	+3	580	6.7e-190	5
pir|S|S29610 parathyroid hormone receptor - h...	+3	580	6.1e-189	5
gp|M77184|RATPATHYR_1 parathyroid hormone receptor [Ra...	+3	576	7.7e-188	5
gp|X78936|MMPHRPR_1 parathyroid hormone/parathyroid ...	+3	576	7.7e-188	5
pir|S|A42698 parathyroid hormone and parathyr...	+3	576	7.7e-188	5
gp|L34611|MUSPTHR06_1 parathyroid hormone/parathyroid ...	+3	576	4.1e-174	5
gp|U11087|HSV1RG9_1 vasoactive intestinal peptide 1 ...	+3	319	1.2e-98	5
gp|M86835|RATVASREC_1 vasoactive intestinal polypeptid...	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana]
            Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG.3A

Match with FIG. 3 A

```
Query:   729  IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT  908
              I +++ +   E     DK+  ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+
Sbjct:   253  ITEEELRAFTEPPPADKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK  312

Query:   909  KYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF  1088
              KYLWGF L GWG PA FVA W  RATLA+  CW+LS+G+ KWI Q PILAAI +NFILF
Sbjct:   313  KYLWGFTLFGWGLPAVFVAVWTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF  372

Query:  1089  LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVFGVHYIVFVCLPHS  1244
              +N +RVLATK+ ETNA    DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
Sbjct:   373  INIIRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHYIVFMATPYT  424
```

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

```
Query:   267  EGNCFPEMDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW  446
              +G C PEMD ++CWP G  GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ +  N+TW
Sbjct:   102  DGFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHKGRAYRRCDSNGSWELVPGNNRTW  161

Query:   447  ANYSDCLRFL  476
              ANYS+C++FL
Sbjct:   162  ANYSECVKFL  171
```

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

```
Query:   498  KQEFCERLYVMYTVGYSISFGSLAVAILIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV  677
              ++E   +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
```

Match with FIG. 3 C

FIG.3B

MATCH WITH FIG. 3B

```
Sbjct:   177  EREVFDRLGMIYTVGYSISLGSLTVAVLILGYFRRLHCTRNYIHMLFVSFMLRAVSIFI 236

Query:   678  KDRVVHAHIGVKELESLIMQD 740
              KD V+++  E+E +  ++
Sbjct:   237  KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query:  1248  TGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS 1424
              +G+ W+++MH E+ FNSFQGFFV+IIYC+CNGEVQAE+KK WSRW L++D+KR    GS
Sbjct:   427  SGILWQVQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query:   159  AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269
              A +D+D  IT EEQI+L+  A+ QCE  +  L+ E
Sbjct:    24  ALVDADDVITKEEQILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query:  1508  ISGKAAKIASRQPDSHITLPGYV 1576
              +S + A  A   + H  LPGYV
Sbjct:   512  LSPRLAPGAGASANGHHQLPGYV 534
```

FIG.3C